

SEQUENCE LISTING

<110> Jegla, Timothy James
ICAgan, Inc.

<120> Human HAC3

<130> 018512-002210US

<140> US 09/548,933
<141> 2000-04-13

<150> US 60/129,456
<151> 1999-04-15

<160> 16

<170> PatentIn Ver. 2.1

<210> 1
<211> 774
<212> PRT
<213> Homo sapiens

<220>
<223> human hyperpolarization-activated voltage-gated
cation channel 3 (HAC3)

<400> 1
Met Glu Ala Glu Glu Gln Arg Pro Ala Ala Gly Ala Ser Glu Gly Ala Thr
1 5 10 15
Pro Gly Leu Glu Ala Val Pro Pro Val Ala Pro Pro Pro Ala Thr Ala
20 25 30
Ala Ser Gly Pro Ile Pro Lys Ser Gly Pro Glu Pro Lys Arg Arg His
35 40 45
Leu Gly Thr Leu Leu Gln Pro Thr Val Asn Lys Phe Ser Leu Arg Val
50 55 60
Phe Gly Ser His Lys Ala Val Glu Ile Glu Gln Glu Arg Val Lys Ser
65 70 75 80
Ala Gly Ala Trp Ile Ile His Pro Tyr Ser Asp Phe Arg Phe Tyr Trp
85 90 95
Asp Leu Ile Met Leu Leu Met Val Gly Asn Leu Ile Val Leu Pro
100 105 110
Val Gly Ile Thr Phe Phe Lys Glu Glu Asn Ser Pro Pro Trp Ile Val
115 120 125
Phe Asn Val Leu Ser Asp Thr Phe Phe Leu Leu Asp Leu Val Leu Asn
130 135 140
Phe Arg Thr Gly Ile Val Val Glu Glu Gly Ala Glu Ile Leu Leu Ala
145 150 155 160
Pro Arg Ala Ile Arg Thr Arg Tyr Leu Arg Thr Trp Phe Leu Val Asp
165 170 175

Leu Ile Ser Ser Ile Pro Val Asp Tyr Ile Phe Leu Val Val Glu Leu
 180 185 190
 Glu Pro Arg Leu Asp Ala Glu Val Tyr Lys Thr Ala Arg Ala Leu Arg
 195 200 205
 Ile Val Arg Phe Thr Lys Ile Leu Ser Leu Leu Arg Leu Leu Arg Leu
 210 215 220
 Ser Arg Leu Ile Arg Tyr Ile His Gln Trp Glu Glu Ile Phe His Met
 225 230 235 240
 Thr Tyr Asp Leu Ala Ser Ala Val Val Arg Ile Phe Asn Leu Ile Gly
 245 250 255
 Met Met Leu Leu Leu Cys His Trp Asp Gly Cys Leu Gln Phe Leu Val
 260 265 270
 Pro Met Leu Gln Asp Phe Pro Pro Asp Cys Trp Val Ser Ile Asn His
 275 280 285
 Met Val Asn His Ser Trp Gly Arg Gln Tyr Ser His Ala Leu Phe Lys
 290 295 300
 Ala Met Ser His Met Leu Cys Ile Gly Tyr Gly Gln Gln Ala Pro Val
 305 310 315 320
 Gly Met Pro Asp Val Trp Leu Thr Met Leu Ser Met Ile Val Gly Ala
 325 330 335
 Thr Cys Tyr Ala Met Phe Ile Gly His Ala Thr Ala Leu Ile Gln Ser
 340 345 350
 Leu Asp Ser Ser Arg Arg Gln Tyr Gln Glu Lys Tyr Lys Gln Val Glu
 355 360 365
 Gln Tyr Met Ser Phe His Lys Leu Pro Ala Asp Thr Arg Gln Arg Ile
 370 375 380
 His Glu Tyr Tyr Glu His Arg Tyr Gln Gly Lys Met Phe Asp Glu Glu
 385 390 395 400
 Ser Ile Leu Gly Glu Leu Ser Glu Pro Leu Arg Glu Glu Ile Ile Asn
 405 410 415
 Phe Thr Cys Arg Gly Leu Val Ala His Met Pro Leu Phe Ala His Ala
 420 425 430
 Asp Pro Ser Phe Val Thr Ala Val Leu Thr Lys Leu Arg Phe Glu Val
 435 440 445
 Phe Gln Pro Gly Asp Leu Val Val Arg Glu Gly Ser Val Gly Arg Lys
 450 455 460
 Met Tyr Phe Ile Gln His Gly Leu Leu Ser Val Leu Ala Arg Gly Ala
 465 470 475 480
 Arg Asp Thr Arg Leu Thr Asp Gly Ser Tyr Phe Gly Glu Ile Cys Leu
 485 490 495

Leu Thr Arg Gly Arg Arg Thr Ala Ser Val Arg Ala Asp Thr Tyr Cys
 500 505 510

Arg Leu Tyr Ser Leu Ser Val Asp His Phe Asn Ala Val Leu Glu Glu
 515 520 525

Phe Pro Met Met Arg Arg Ala Phe Glu Thr Val Ala Met Asp Arg Leu
 530 535 540

Leu Arg Ile Gly Lys Lys Asn Ser Ile Leu Gln Arg Lys Arg Ser Glu
 545 550 555 560

Pro Ser Pro Gly Ser Ser Gly Gly Ile Met Glu Gln His Leu Val Gln
 565 570 575

His Asp Arg Asp Met Ala Arg Gly Val Arg Gly Arg Ala Pro Ser Thr
 580 585 590

Gly Ala Gln Leu Ser Gly Lys Pro Val Leu Trp Glu Pro Leu Val His
 595 600 605

Ala Pro Leu Gln Ala Ala Ala Val Thr Ser Asn Val Ala Ile Ala Leu
 610 615 620

Thr His Gln Arg Gly Pro Leu Pro Leu Ser Pro Asp Ser Pro Ala Thr
 625 630 635 640

Leu Leu Ala Arg Ser Ala Trp Arg Ser Ala Gly Ser Pro Ala Ser Pro
 645 650 655

Leu Val Pro Val Arg Ala Gly Pro Trp Ala Ser Thr Ser Arg Leu Pro
 660 665 670

Ala Pro Pro Ala Arg Thr Leu His Ala Ser Leu Ser Arg Ala Gly Arg
 675 680 685

Ser Gln Val Ser Leu Leu Gly Pro Pro Pro Gly Gly Gly Arg Arg
 690 695 700

Leu Gly Pro Arg Gly Arg Pro Leu Ser Ala Ser Gln Pro Ser Leu Pro
 705 710 715 720

Gln Arg Ala Thr Gly Asp Gly Ser Pro Gly Arg Lys Gly Ser Gly Ser
 725 730 735

Glu Arg Leu Pro Pro Ser Gly Leu Leu Ala Lys Pro Pro Arg Thr Ala
 740 745 750

Gln Pro Pro Arg Pro Pro Val Pro Glu Pro Ala Thr Pro Arg Gly Leu
 755 760 765

Gln Leu Ser Ala Asn Met
 770

<210> 2
<211> 2325
<212> DNA
<213> Homo sapiens

<220>

<223> human hyperpolarization-activated voltage-gated
cation channel 3 (HAC3)

<400> 2

atggaggcag agcagcggcc ggccggcgcccc gcccggcaag gggcgacccc tggactggag 60
 gcgggtgcctc ccgttgctcc cccgcctgct accgcggccct cagggtccat ccccaaattct 120
 gggcctgagc ctaagaggag gcaccttggg acgtgtctcc agcctacggt caacaagttc 180
 tcccttcggg tggttcggcag ccacaaagca gtggaaatcg agcaggagcg ggtgaagtca 240
 gcggggggcct ggatcatcca cccctacagc gacttccggt ttacttgggat cctgatcatg 300
 ctgctgctga tggtggggaa cctcatcgcc ctgcctgtgg gcatcacctt cttcaaggag 360
 gagaactccc cgcccttggat cgtcttcaac gtattgtctg atacttctt cctactggat 420
 ctgggtctca acttccgaac gggcatcggt gtggaggagg gtgctgagat cctgctggca 480
 cccggggcca tccgcacgctg ctaccctgcgc acatggttcc tgggttgcacat cttctttct 540
 atccctgtgg attacatctt ccttagtggg gagctggagc cacggttgga cgctgaggtc 600
 tacaacacgg cacggccct acgcacatcggt cgcttcacca agatcctaag cctgctgagg 660
 ctgctccgccc tctccgcct catccgctac atacaccagt gggaggagat ctttcacatg 720
 acctatgacc tggccagtgc tgggttgcgc atcttcaacc tcattggat gatgctgctg 780
 ctatgtcaact gggatggctg tctgcagttc ctgggtggcca tgctgcagga ctccctccc 840
 gactgttggg tctccatcaa ccacatggtg aaccactcggt gggggccca gtattccat 900
 gccctgttca aggccatgag ccacatcggt tgcatggct atgggcagca ggcacctgt 960
 ggcacatggc acgtctggct caccatcgctc agcatgatcg taggtgccac atgctacgcc 1020
 atgttcatcg gccatgccac ggcactcatc cagtcctgg actcttcccg gctcagttac 1080
 caggagaagt acaagcaggta ggagcagttc atgtccttcc acaagctgcc agcagacacg 1140
 cggcagcgca tccacacgta ctatgagcac cgctaccagg gcaagatgtt cgatgaggaa 1200
 agcatcctgg gcgagctgag cgacccgctt cgcgaggaga tcattaactt cacctgtcgg 1260
 ggcctgggtgg cccacatgcc gctgtttgcc catgccgacc ccagcttcgt cactgcagtt 1320
 ctcaccaaggc tgctgttgc ggtcttccag ccgggggatc tgctgttgc tgagggtctcc 1380
 gtggggagga agatgtactt catccagcat gggctgtca gtgtgttgc cccggccggcc 1440
 cgggacacac gcctcaccga tggatcctac tttggggaga tctgcctgt aactaggggc 1500
 cggcgcacag ccagtgttcg ggctgacacc tactgccgccc ttacttcaact cagcgtggac 1560
 catttcaatgc ctgtgttgc ggagttcccc atgatgcgcc gggccttgc gactgtggcc 1620
 atggatcgcc tgctccgcat cggcaagaag aattccatac tgcaaggaa ggcctccgag 1680
 ccaagtcacag gcagcagtgg tggcatcatg gaggacact tgggtcaaca tgacagagac 1740
 atggctcggg gtgttgggg tcggggccccg agcacaggag ctcagcttag tggaaagcca 1800
 gtactgtggg agccactggc acatgcgcc cttcaggcag tgctgtgac ctccaatgtg 1860
 gccattgccc tgactcatca gggggccct ctggccctct cccctgactc tccagccacc 1920
 ctccttgctc gctctgttgc ggcgtcagca ggctctccag ctcccccgct ggtgcccgtc 1980
 cgagctggcc catggcattc cacctccgc ctggccgccc cacctggccg aaccctgcac 2040
 gccagccat cccggcagg ggcgtccccg gtctccctgc tgggtcccccc tccaggagga 2100
 ggtggacggc ggctaggacc tcggggccgc ccactctcag ctcctccaaacc ctctctgcct 2160
 cagcggggca caggcgtatgg ctctcttggg cgttaaggat caggaagtga gcccgtgcct 2220
 ccctcaggcgc tcctggccaa acctccaagg acagcccagc ccccccaggcc accagtgcct 2280
 gagccagcca cacccgggg tctccagctt tctgccaaca tgtaa 2325

<210> 3

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:amplification
primer

<400> 3

cagccatggc ggcagagcag cggc

<210> 4
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:amplification primer

<400> 4
ggaggagatc tttcacatga catacgac

28

<210> 5
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:amplification primer

<400> 5
agttaggatcc atcggtgagg cgtg

24

<210> 6
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:amplification primer

<400> 6
ttacatgttg gcagaaagct ggagacc

27

<210> 7
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:degenerate amplification primer

<220>
<221> modified_base
<222> (24)
<223> n = g, a, c or t

<400> 7
tg.gaggaga tcttgcayat gacntayga

29

<210> 8
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:degenerate
amplification primer

<220>
<221> modified_base
<222> (16)
<223> n = g, a, c or t

<220>
<221> modified_base
<222> (25)
<223> n = g, a, c or t

<400> 8
cgtctcgaaat gcccknckca tcatngg

27

<210> 9
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:first round 5'
RACE gene specific primer

<400> 9
cctgctgccc atagccaatg cacagc

26

<210> 10
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:second round
nested 5' RACE gene specific primer

<400> 10
gcaccacgaa ctgcagacag ccatc

25

<210> 11
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nested 3' RACE
gene specific reamplification primer

<400> 11
gttctcacca agctgcgcctt tgaggta

27

<210> 12
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nested 3' RACE
gene specific primer

<400> 12
ccagcatggg ctgctcagtg tgctg

25

<210> 13
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nested 3' RACE
gene specific primer

<400> 13
gcccaactctc agcctcccaa ccctc

25

<210> 14
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nested 3' RACE
gene specific primer

<400> 14
cccaaccaag cttgcctcag cgggcaacag gcgatgg

37

<210> 15
<211> 875
<212> PRT
<213> Homo sapiens

<220>
<223> human hyperpolarization-activated voltage-gated
cation channel 1 (HAC1)

<400> 15
Met Asp Ala Arg Gly Gly Gly Arg Pro Gly Glu Ser Pro Gly Ala
1 5 10 15

Thr Pro Ala Pro Gly Pro Pro Pro Pro Pro Ala Pro Pro Pro Gly
20 25 30

Pro Gly Pro Ala Pro Pro Gln His Pro Pro Arg Ala Glu Ala Leu Pro
35 40 45

Pro Glu Ala Ala Asp Glu Gly Gly Pro Arg Gly Arg Leu Arg Ser Arg
50 55 60

Asp Ser Ser Cys Gly Arg Pro Gly Thr Pro Gly Ala Ala Ser Thr Ala
65 70 75 80

Lys Gly Ser Pro Asn Gly Glu Cys Gly Arg Gly Glu Pro Gln Cys Ser
85 90 95

Pro Ala Gly Pro Glu Gly Pro Ala Arg Gly Pro Lys Val Ser Phe Ser
 100 105 110
 Cys Arg Gly Ala Ala Ser Gly Pro Ala Pro Gly Pro Gly Pro Ala Glu
 115 120 125
 Glu Ala Gly Ser Glu Glu Ala Gly Pro Ala Gly Glu Pro Arg Gly Ser
 130 135 140
 Gln Ala Ser Phe Met Gln Arg Gln Phe Gly Ala Leu Leu Gln Pro Gly
 145 150 155 160
 Val Asn Lys Phe Ser Leu Arg Met Phe Gly Ser Gln Lys Ala Val Glu
 165 170 175
 Arg Glu Gln Glu Arg Val Lys Ser Ala Gly Ala Trp Ile Ile His Pro
 180 185 190
 Tyr Ser Asp Phe Arg Phe Tyr Trp Asp Phe Thr Met Leu Leu Phe Met
 195 200 205
 Val Gly Asn Leu Ile Ile Ile Pro Val Gly Ile Thr Phe Phe Lys Asp
 210 215 220
 Glu Thr Thr Ala Pro Trp Ile Val Phe Asn Val Val Ser Asp Thr Phe
 225 230 235 240
 Phe Leu Met Asp Leu Val Leu Asn Phe Arg Thr Gly Ile Val Ile Glu
 245 250 255
 Asp Asn Thr Glu Ile Ile Leu Asp Pro Glu Lys Ile Lys Lys Tyr
 260 265 270
 Leu Arg Thr Trp Phe Val Val Asp Phe Val Ser Ser Ile Pro Val Asp
 275 280 285
 Tyr Ile Phe Leu Ile Val Glu Lys Gly Ile Asp Ser Glu Val Tyr Lys
 290 295 300
 Thr Ala Arg Ala Leu Arg Ile Val Arg Phe Thr Lys Ile Leu Ser Leu
 305 310 315 320
 Leu Arg Leu Leu Arg Leu Ser Arg Leu Ile Arg Tyr Ile His Gln Trp
 325 330 335
 Glu Glu Ile Phe His Met Thr Tyr Asp Leu Ala Ser Ala Val Met Arg
 340 345 350
 Ile Cys Asn Leu Ile Ser Met Met Leu Leu Leu Cys His Trp Asp Phe
 355 360 365
 Cys Leu Gln Phe Leu Val Pro Met Leu Gln Asp Phe Pro Arg Asn Cys
 370 375 380
 Trp Val Ser Ile Asn Gly Met Val Asn His Ser Trp Ser Glu Leu Tyr
 385 390 395 400
 Ser Phe Ala Leu Phe Lys Ala Met Ser His Met Leu Cys Ile Gly Tyr
 405 410 415

Gly Arg Gln Ala Pro Glu Ser Met Thr Asp Ile Trp Leu Thr Met Leu
 420 425 430
 Ser Met Ile Val Gly Ala Thr Cys Tyr Ala Met Phe Ile Gly His Ala
 435 440 445
 Thr Ala Leu Ile Gln Ser Leu Asp Ser Ser Arg Arg Gln Tyr Gln Glu
 450 455 460
 Lys Tyr Lys Gln Val Glu Gln Tyr Met Ser Phe His Lys Leu Pro Ala
 465 470 475 480
 Asp Phe Arg Gln Lys Ile His Asp Tyr Tyr Glu His Arg Tyr Gln Gly
 485 490 495
 Lys Met Phe Asp Glu Asp Ser Ile Leu Gly Glu Leu Asn Gly Pro Leu
 500 505 510
 Arg Glu Glu Ile Val Asn Phe Asn Cys Arg Lys Leu Val Ala Ser Met
 515 520 525
 Pro Leu Phe Ala Asn Ala Asp Pro Asn Phe Val Thr Ala Met Leu Thr
 530 535 540
 Lys Leu Lys Phe Glu Val Phe Gln Pro Gly Asp Tyr Ile Ile Arg Glu
 545 550 555 560
 Gly Thr Ile Gly Lys Lys Met Tyr Phe Ile Glx His Gly Val Val Ser
 565 570 575
 Val Leu Thr Lys Gly Asn Lys Glu Met Lys Leu Ser Asp Gly Ser Tyr
 580 585 590
 Phe Gly Glu Ile Cys Leu Leu Thr Arg Gly Arg Arg Thr Ala Ser Val
 595 600 605
 Arg Ala Asp Thr Tyr Cys Arg Leu Tyr Ser Leu Ser Val Asp Asn Phe
 610 615 620
 Asn Glu Val Leu Glu Glu Tyr Pro Met Met Arg Arg Ala Phe Glu Thr
 625 630 635 640
 Val Ala Ile Asp Arg Leu Asp Arg Ile Gly Lys Lys Asn Ser Ile Leu
 645 650 655
 Leu His Lys Val Gln His Asp Leu Asn Ser Gly Val Phe Asn Asn Gln
 660 665 670
 Glu Asn Ala Ile Ile Gln Glu Ile Val Lys Tyr Asp Arg Glu Met Val
 675 680 685
 Gln Gln Ala Glu Leu Gly Gln Arg Val Gly Leu Phe Pro Pro Pro
 690 695 700
 Pro Pro Pro Gln Val Thr Ser Ala Ile Ala Thr Leu Gln Gln Ala Ala
 705 710 715 720
 Ala Met Ser Phe Cys Pro Gln Val Ala Arg Pro Leu Val Gly Pro Leu
 725 730 735

Ala Leu Gly Ser Pro Arg Leu Val Arg Arg Pro Pro Pro Gly Pro Ala
 740 745 750

Pro Ala Ala Ala Ser Pro Gly Pro Pro Pro Ala Ser Pro Pro Gly
 755 760 765

Ala Pro Ala Ser Pro Arg Ala Pro Arg Thr Ser Pro Tyr Gly Gly Leu
 770 775 780

Pro Ala Ala Pro Leu Ala Gly Pro Ala Leu Pro Ala Arg Arg Leu Ser
 785 790 800

Arg Ala Ser Arg Pro Leu Ser Ala Ser Gln Pro Ser Leu Pro His Gly
 805 810 815

Ala Pro Gly Pro Ala Ala Ser Thr Arg Pro Ala Ser Ser Ser Thr Pro
 820 825 830

Arg Leu Gly Pro Thr Pro Ala Ala Arg Ala Ala Ala Pro Ser Pro Asp
 835 840 845

Arg Arg Asp Ser Ala Ser Pro Gly Ala Ala Gly Gly Leu Asp Pro Gln
 850 855 860

Asp Ser Ala Arg Ser Arg Leu Ser Ser Asn Leu
 865 870 875

<210> 16

<211> 749

<212> PRT

<213> Homo sapiens

<220>

<223> human hyperpolarization-activated voltage-gated
 cation channel 2 (HAC2) missing amino terminus

<400> 16

Lys Glu Gln Glu Arg Val Lys Thr Ala Gly Phe Trp Ile Ile His Pro
 1 5 10 15

Tyr Ser Asp Phe Arg Phe Tyr Trp Asp Leu Ile Met Leu Ile Met Met
 20 25 30

Val Gly Asn Leu Val Ile Ile Pro Val Gly Ile Thr Phe Phe Thr Glu
 35 40 45

Gln Thr Thr Pro Trp Ile Ile Phe Asn Val Ala Ser Asp Thr Val
 50 55 60

Phe Leu Leu Asp Leu Ile Met Asn Phe Arg Thr Gly Thr Val Asn Glu
 65 70 75 80

Asp Ser Ser Glu Ile Ile Leu Asp Pro Lys Val Ile Lys Met Asn Tyr
 85 90 95

Leu Lys Ser Trp Phe Val Val Asp Phe Ile Ser Ser Ile Pro Val Asp
 100 105 110

Tyr Ile Phe Leu Ile Val Glu Lys Gly Met Asp Ser Glu Val Tyr Lys
 115 120 125

Thr Ala Arg Ala Leu Arg Ile Val Arg Phe Thr Lys Ile Leu Ser Leu
 130 135 140

Leu Arg Leu Leu Arg Leu Ser Arg Leu Ile Arg Tyr Ile His Gln Trp
 145 150 155 160

Glu Glu Ile Phe His Met Thr Tyr Asp Leu Ala Ser Ala Val Val Arg
 165 170 175

Ile Phe Asn Leu Ile Gly Met Met Leu Leu Leu Cys His Trp Asp Phe
 180 185 190

Cys Leu Gln Phe Leu Val Pro Leu Leu Gln Asp Phe Pro Pro Asp Cys
 195 200 205

Trp Val Ser Leu Asn Glu Met Val Asn Asp Ser Trp Gly Lys Gln Tyr
 210 215 220

Ser Tyr Ala Leu Phe Lys Ala Met Ser His Met Leu Cys Ile Gly Tyr
 225 230 235 240

Gly Ala Gln Ala Pro Val Ser Met Ser Asp Leu Trp Ile Thr Met Leu
 245 250 255

Ser Met Ile Val Gly Ala Thr Cys Tyr Ala Met Phe Val Gly His Ala
 260 265 270

Thr Ala Leu Ile Gln Ser Leu Asp Ser Ser Arg Arg Gln Tyr Gln Glu
 275 280 285

Lys Tyr Lys Gln Val Glu Gln Tyr Met Ser Phe His Lys Leu Pro Ala
 290 295 300

Asp Met Arg Gln Lys Ile His Asp Tyr Tyr Glu His Arg Tyr Gln Gly
 305 310 315 320

Lys Ile Phe Asp Glu Glu Asn Ile Leu Asn Glu Leu Asn Asp Pro Leu
 325 330 335

Arg Glu Glu Ile Val Asn Phe Asn Cys Arg Lys Leu Val Ala Thr Met
 340 345 350

Pro Leu Phe Ala Asn Ala Asp Pro Asn Phe Val Thr Ala Met Leu Ser
 355 360 365

Lys Leu Arg Phe Glu Val Phe Gln Pro Gly Asp Tyr Ile Ile Arg Glu
 370 375 380

Gly Ala Val Gly Lys Lys Met Tyr Phe Ile Glx His Gly Val Ala Gly
 385 390 395 400

Val Ile Thr Lys Ser Ser Lys Glu Met Lys Leu Thr Asp Gly Ser Tyr
 405 410 415

Phe Gly Glu Ile Cys Leu Leu Thr Lys Gly Arg Arg Thr Ala Ser Val
 420 425 430

Arg Ala Asp Thr Tyr Cys Arg Leu Tyr Ser Leu Ser Val Asp Asn Phe
 435 440 445

Asn Glu Val Leu Glu Glu Tyr Pro Met Met Arg Arg Ala Phe Glu Thr
 450 455 460
 Val Ala Ile Asp Arg Leu Asp Arg Ile Gly Lys Lys Asn Ser Ile Leu
 465 470 475 480
 Leu Gln Lys Phe Gln Lys Asp Leu Asn Thr Gly Val Phe Asn Asn Gln
 485 490 495
 Glu Asn Glu Ile Leu Lys Gln Ile Val Lys His Asp Arg Glu Met Val
 500 505 510
 Gln Ala Ile Ala Pro Ile Asn Tyr Pro Gln Met Thr Thr Leu Asn Ser
 515 520 525
 Thr Ser Ser Thr Thr Pro Thr Ser Arg Met Arg Thr Gln Ser Pro
 530 535 540
 Pro Val Tyr Thr Ala Thr Ser Leu Ser His Ser Asn Leu His Ser Pro
 545 550 555 560
 Ser Pro Ser Thr Gln Thr Pro Gln Pro Ser Ala Ile Leu Ser Pro Cys
 565 570 575
 Ser Tyr Thr Thr Ala Val Cys Ser Pro Pro Val Gln Ser Pro Leu Ala
 580 585 590
 Ala Arg Thr Phe His Tyr Ala Ser Pro Thr Ala Ser Gln Leu Ser Leu
 595 600 605
 Met Gln Gln Gln Pro Gln Gln Gln Val Gln Gln Ser Gln Pro Pro Gln
 610 615 620
 Arg Gln Pro Gln Gln Pro Ser Pro Gln Pro Gln Thr Pro Gly Ser Ser
 625 630 635 640
 Thr Pro Lys Asn Glu Val His Lys Ser Thr Gln Ala Leu His Asn Thr
 645 650 655
 Asn Leu Thr Arg Glu Val Arg Pro Phe Ser Ala Trp Gln Pro Ser Leu
 660 665 670
 Pro His Glu Val Ser Thr Leu Ile Ser Arg Pro His Pro Thr Val Gly
 675 680 685
 Glu Ser Leu Ala Ser Ile Pro Gln Pro Val Thr Ala Val Pro Gly Thr
 690 695 700
 Gly Leu Gln Ala Gly Gly Arg Ser Thr Val Pro Gln Arg Val Thr Phe
 705 710 715 720
 Phe Arg Gln Met Ser Ser Gly Ala Ile Pro Pro Asn Arg Gly Val Leu
 725 730 735
 Pro Ala Pro Leu Pro Leu Ile Thr Pro His Pro Lys Lys
 740 745